An Adaptive Knowledge Representation System for Genomics

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The rapid proliferation of web-based information and communication technologies significantly changes ways to view information systems and represents the early stages of a global information server. This change is even more significant in scientific domains, such as genomics and proteomics, where pieces of information are dispersed in a large variety of data sources. Ideally, we can imagine an information based society as a unit, where the users will obtain relevant answers to their questions, process reliable data and collaborate and share knowledge with each other as well. We will stay humble in regards to the semantic, syntactic, political and social challenges that are raised by this ideal, and just focus in detail on semantic and syntactic issues.

It is a fact that we definitely need intelligent knowledge organization. Some people will speak about a connective tissue, others about a shared conceptualization (ontology) and still others about a federal scheme. It is an other fact that we also need a close interation between the users and the system. This interaction is specially focused on the system architecture and the dialogs between software and users. In our opinion, graphical user interfaces have to be tailored specifically to make the system appropriate for all the users. In particular, interfaces have to offer powerful adaptational and evolutional properties, to be capable of acting as a mediator between one or more humans and one or more computational machines.

Our interests are focused on interactivity, more specifically on adaptive interactivity. In addition we assume that interactivity is connected with the building of an adaptive interface and interactive ontology. In our opinion, these two critical tasks are dependent on each other and considered as a unit. We are currently developing an appropriate system, which offers powerful adaptational and evolutional properties to the human-computer interface. That gives the users an active role in the ontology building.

Consequently, we base our development on some of our research tools, which enable collaborative browsing, creation and editing of ontologies. A problem occurs for a user, when an ambiguity appears in a classification or an object description. Removal of the ambiguity from knowledge bases clearly requires interaction between humans and computers. Furthermore, the ambiguity may have different effects. For instance, a new user or a piece of information forces an inductive revision of the knowledge base, and occasionally an abductive revision by drastic modifications of the conceptual schema. To assist adaptation and revision of an ontology, we are currently developing tools that are based on learning mechanisms and constraint propagation on a hierarchy of types.

Our research aims to respond to numerous problems users and biologists in particular face when searching information on the Web. In particular, biologists ask for relevant and valid information. One of the main objectives of such an approach is to identify and deliver high quality information. The system will give biologists the possibility to estimate the reliability of data, and by this means keep control of their analysis. The user (biologist) will play a core role. His/her context of work, as well as his/her needs or interests, will be used to refine the global ontology and as a result the system. Consequently the user will obtain a resource or a service with the highest flexibility and security standards.